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ORIGINAL PAPER

Genetic evaluation of twenty seed sources of *Asparagus racemosus*

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Abstract: A field trial of 20 seed sources of *Asparagus racemosus* was conducted at the Forest Research Institute, Dehradun, Uttarakhand, India to evaluate their performance of different economic traits. Genotypic variance, phenotypic variance, genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) for number of shoots, shoot height, shoot weight, number of roots, root length, root diameter and root weight were calculated. Maximum genotypic and phenotypic variance was observed in shoot height among the shoot - related traits and root length among the root - related traits. For the shoot height, genotypic variance, phenotypic variance, genotypic coefficient of variance, phenotypic coefficient of variance were 231.80, 3924.80, 61.26 and 1037.32, respectively, where those of the root length were 9.55, 16.80, 23.46 and 41.27, respectively. The maximum genetic advance and genetic gain were obtained for shoot height among the shoot-related traits and root length among the root-related traits. Index values were developed for all the seed sources based on the four most important traits, and Panthnagar (Uttrakhand), Jodhpur (Rajasthan), Dehradun (Uttarakhand), Chandigarh (Punjab), Jammu (Jammu and Kashmir) and Solan (Himachal Pradesh), were promising seed sources for root production.

Keywords: *Asparagus racemosus*; genetic advance; genetic gain; heritability; index selection; seed sources

Introduction

Asparagus racemosus Willd. is an important medicinal plant commonly known as Shatawari. It is the main Ayurvedic medicinal tonic especially for the female, as is *Withania somnifera* for the male. *A. racemosus* is known to improve the defense mechanisms of the body and enhance longitivity (Bhattacharya et al. 2000) and most of the tribes and rural communities use it for diabetes (Rana et al. 1999). The roots are used mainly to promote the secretion of milk and improve reduced body weight and considered as an aphrodisiac. The methanol extracted from its roots is found to have *in vitro* antibacterial efficacy against *Escherichia coli*, *Shigella flexneri*, *Vibrio cholerae, Salmonella typhi, Salmoneela typhimurium, Pseudomonas putida, Bacilus subtilis* and *Staphylococcus aureus* (Mandal et al. 2000). Detailed exploration pharmacological properties of the root extract of *A. racemosus* has been reviewed by Goyal et al. (2003). Owing to increased demand, the species has attracted the attention for its genetic improvement, conservation and cultivation. It is one of the 32 plant species that have been identified as priority species for cultivation and conservation by National Medicinal Plant Board (NMPB), Ministry for Health and Family Welfare, Government of India, New Delhi, India (Kala and Sajwan 2007).

Genetic diversity through random amplified polymorphic DNA (RAPD) markers has been studied in *A. racemosus*. High level of genetic similarity was observed in accessions collected from Madhya Pradesh, India (Vijay et al. 2009) as well as Himanchal Pradesh and Tamil Nadu (Ginwal et al. 2009). However, a very little attention is being paid towards its genetic improvement and selection of desired types with higher performance in traits of economic importance. It is therefore important to find out the phenotypic variation in different seed sources for economic characters and evaluate such genetic parameters as heritability, genetic gain and genetic correlation. The objectives of this study were to select promising seed sources for multiplication and provide the base material for further improvement practices including hybridization.

Materials and methods

The seeds of *A. racemosus* were collected from 20 different geographical regions emanating from 10 states of India *viz*. Haryana, Punjab, Jammu & Kashmir (J&K), Himachal Pradesh (H.P.), Rajasthan, Madhya Pradesh (M.P.), Uttarakhand, Bihar, New Delhi and Tamil Nadu (Table 1). The germplasm collected was established in the germplasm bank at the Forest Research Institute, Dehradun (Uttarakhand), India. The seedlings for establish-

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ing the evaluation trial were raised in a uniform manner for all seed sources.

Table 1. List of seed sources for field evaluation

S. No.	Source	State	Latitude	Longitude
1.	Jodhpur (1)	Rajasthan	26º 18' N	73º 04' E
2.	Jodhpur (2)	Rajasthan	26º 18' N	73º 04' E
3.	Dehradun	Uttarakhand	30º 19' N	78º 04' E
4.	Jabalpur	Madhya Pradesh	23º 10' N	79º 59' E
5.	Ambikapur	Madhya Pradesh	23º 10' N	83º 15' E
6.	Chandigarh	Punjab	30º 42' N	76º 54' E
7.	Pantnagar	Uttarakhand	29º 58' N	78º 13' E
8.	Chitrakoot	Madhya Pradesh	29º 05' N	79º 51' E
9.	Hissar	Haryana	29º 10' N	75º 46' E
10.	Jammu	Jammu & Kashmir	32º 43' N	74º 54' E
11.	Mandi	Himachal Pradesh	31º 43' N	76º 58' E
12.	Rishikesh	Uttarakhand	30º 11' N	75º 31' E
13.	Solan	Himachal Pradesh	30º 55' N	77º 70' E
14.	Kolapa-kkam	Tamil Nadu	12º 87' N	80º 10' E
15.	Anupuram	Tamil Nadu	12º 42' N	80º 01' E
16.	Tambaram	Tamil Nadu	13º 04' N	80º 17' E
17.	Rishikesh	Uttarakhand	30º 11' N	78º 31' E
18.	NBPGR	New Delhi	28º 38' N	77º 12' E
19.	Ajmer	Rajasthan	26º 27' N	74º 42' E
20.	Yamuna Nagar	Haryana	30º 60' N	77º 16' E

Establishment of field trial

The field trial was established in a randomized block design with three replications and nine plants in a plot for evaluation of the growth performance, totaling to 27 plants in each treatment. Six-month-old seedlings were planted in the field with pit size 45 cm × 45 cm × 45 cm and a uniform spacing of 1 m × 1 m. Data were recorded at the age of one and a half years on the morphological traits of the seedlings including number of shoot, shoot height, shoot weight, number of roots, root length, root diameter and root weight of each plant. No fertilizers were provided to the plants.

Statistical analysis

Analysis of variability: The observations were subject to analysis of variance as described by Sukhatme and Amble (1989). The significance of difference among treatment means was estimated using `F' test.

Variance: The genotypic and phenotypic components of variance for various traits were calculated from the ANOVA analysis as described by Burton (1952).

(1) *Genotypic variance* $(\sigma^2 g) = (\sigma^2{}_c - \sigma^2{}_e)/r$, where $\sigma^2{}_c$ is genotypic mean squares, $\sigma^2{}_e$ is error mean squares and r is number of replications.

(2) *Phenotypic variance* $(\sigma^2 p) = \sigma^2 g + \sigma^2{}_e$, where $\sigma^2 g$ is the genotypic variance and $\sigma^2 e$ is error mean squares.

(3) *Coefficient of variance:* genotypic coefficient of variance (GCV) was estimated using the following formula (Burton 1952). GCV = $(\sqrt{\sigma^2 g} \times 100)$/mean, where $\sigma^2 g$ = genotypic variance

(4) *Phenotypic coefficient of variance (PCV)* was calculated using the following formula (Burton 1952). PCV = $(\sqrt{\sigma^2 p} \times 100)$/mean, where $\sigma^2 p$ = Phenotypic variance.

(5) *Heritability*: Heritability in broad sense (h^2) was calculated using following formula (Lush 1949). $h^2 = \sigma^2 g/\sigma^2 p$, where σ^2_g is genotypic variance and σ^2_p is phenotypic variance.

(6) *Genetic advance:* The genetic advance was calculated as described by Johnson et al. (1955) for all the characters studied. Genetic advance (Gs) = $K \cdot h^2 \cdot \sqrt{\sigma^2_p}$, where K is the selection differential (2.06 at 5% selection intensity as per Cotterill and Dean 1990), h^2 is the heritability (broad sense) and $\sqrt{\sigma^2_p}$ is Phenotypic standard deviation).

(7) *Genetic gain:* The expected genetic gain, in per cent of mean, was calculated following Burton and Devane (1953). Genetic gain = (*Gs* / mean) × 100, where *Gs* = Genetic Advance

Correlation coefficient: The correlation among the traits was analyzed to find out the relationship of one trait and its influence on other traits using SAS (version 9.1.2 software for Windows).

Development of index value: The total index value was developed on the basis of performance of four most important characters *viz*. number of shoots, shoot dry weight, number of roots and root dry weight to select the promising sources using following criterion.

Superiority status	No. of shoots	Shoot dry weight	No. of roots	Root dry weight
> 20 % the average	20	30	20	30
> 10 % the average	15	20	15	20
Average	10	15	10	15
< 10 % the average	5	10	5	10
< 20 % the average	1	1	1	1

Result and discussion

The growth data collected for the 20 seed sources (Table 1) were statistically analyzed. The maximum critical difference (CD) was observed for root production (0.91), followed by root diameter (0.68) and shoot weight (0.49), whereas the minimum CD was observed for root length (0.15) (Table 2). The analysis of variance (ANOVA) showed that all the traits observed were significant among seed sources at 0.01 level of probability (Table 3).

Table 2. General statistics for the seven traits in *A. racemosus*

Static	No. of shoots	Shoot height (cm)	Shoot weight (kg)	No. of roots	Root length (cm)	Root diameter (mm)	Root weight (kg)
Average	20.47	189.18	109.27	20.36	10.63	1.81	1.38
Maximum	48.00	350.00	254.00	40.00	14.00	4.18	6.79
Minimum	8.00	29.2.00	28.00	10.00	6.30	0.32	0.06
Std. Dev	8.80	74.56	53.92	7.96	1.63	1.24	1.26
Critical difference	0.42	0.39	0.49	0.39	0.15	0.68	0.91

Table 3. ANOVA analysis for the seven traits in *A. racemosus*

Traits	Degree of freedom	Sum of squares	Mean sum of squares	
			Seed source	Residual
No. of shoots	19	11.22	0.70**	0.55
Shoot height	19	77640	4852**	3693
Shoot weight	19	21.54	1.35**	1.08
No. of roots	19	72.57	6.54**	1.73
Root length	19	880.26	55.02**	7.25
Root diameter	19	45.07	2.82**	0.56
Root weight	19	14.75	0.92**	0.15

** Significant at .01 level of significance

Genotypic variance, phenotypic variance, genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) were derived from all the traits (Table 4). The maximum genotypic and phenotypic variance as well as GCV and PCV were found for shoot height. Though all root-related traits had higher values of heritability ranging from 0.36 to 0.57, the highest genetic advance (308.29) and genetic gain (162.96) were reported for shoot height. The other two important traits *viz*. root length and root weight had genetic gain of 62.41 and 11.28 %, respectively (Table 5). The correlations among seven traits of growth and root development are presented in Table 6. The maximum significant correlation was found between shoot height and number of roots (0.64) followed by between shoot dry weight and root length (0.64) and between number of roots and root dry weight (0.56). Importantly, there was significant negative correlation between root diameter and number of roots (-0.47).

Table 4. Components of variance for the seven traits in *A. racemosus*

Character	Genotypic variance	Phenotypic variance	Genotypic coefficient of variance	Phenotypic coefficient of variance
No. of shoots	0.03	0.58	0.07	1.42
Shoot height	231.8	3924.8	61.26	1037.32
Shoot weight	0.05	1.13	1.92	41
No. of roots	0.96	2.69	0.44	1.23
Root length	9.55	16.8	23.46	41.27
Root diameter	0.45	1.01	2.12	4.77
Root weight	0.15	0.31	4.24	8.5

Table 5. Genetic parameters for the seven traits in *A. racemosus*

Character	Heritability (broad sense)	Genetic advance	% Genetic gain
No. of shoots	0.05	0.04	0.19
Shoot height	0.06	308.29	162.96
Shoot weight	0.05	0.07	5.1
No. of roots	0.36	1.28	1.17
Root length	0.57	12.71	62.41
Root diameter	0.44	0.6	5.64
Root weight	0.50	0.2	11.28

The genetic parameters are extremely important in predicting the amount of genetic gain to be expected from an improvement programme (Kumar 2007; Kumar et al. 2010). The variation among the seed sources is commonly used as an estimate of the total genetic variation and for calculation of the degree of genetic control for a particular character (Foster and Shaw 1988). The present analysis indicated that it could be possible to select potential seed sources with greater genetic gain for commercially important traits. Hodge et al. (2002) used GCV to express the genetic gain in case of *Bombacopsis quinata*. In this study the large amount of variation observed in all traits offers an ample scope for a breeder to enforce further genetic improvement.

Table 6. Correlations among seven traits in *A. racemosus*

Traits	NS	DWS	SH	NR	RL	RD	DWR
NS	-						
DWS	0.64**	-					
SH	0.39	0.43	-				
NR	0.42	0.39	0.64**	-			
RL	0.43	0.62**	0.26	-0.03	-		
RD	-0.40	-0.40	0.01	-0.47*	0.10	-	
DWR	0.10	0.17	0.40	0.56**	-0.07	-0.40	-

** Significant at 0.01 level of significance; *Significant at 0.05 level of significance. NS-- No. of shoots, DWS-- Dry weight of shoots, SH-- Shoot height, NR-- No. of roots, RL-- Root length, RD-- root diameter, DWR-- Dry weight of roots

It is obvious from the literature that not much work on the genetic improvement of *A. racemosus* has been carried out. The root-related characters, which influence economics of cultivation of the species, had moderate to high broad-sense heritability than that of the shoot-related characters (Table 5). These estimates will guide the selection on the basis of positive genetic response that can be expected at reasonable selection intensity. An important objective of plant improvement programs is to obtain a significant amount of genetic gain at a reasonable cost while maintaining sufficient genetic variability in the breeding population to ensure future gain (Zobel and Talbert 1984). This is accomplished by selecting plants possessing phenotypic characteristic of economic importance and using them as parents in a breeding programme. The index values were calculated for all the seed sources on the basis of field performance (Table 7). In term of index value the maximum index value was observed for Pantnagar (Uttarakhand) seed source followed by Jodhpur (1) (Rajasthan), Dehradun (Uttarakhand), Chandigarh, (Punjab), Jammu (Jammu and Kashmir), Jodhpur (2) (Rajasthan) and Solan (Himachal Pradesh). Genetic diversity through RAPD markers has been studied in *A. racemosus*. High level of genetic similarity was observed in accessions collected from Madhya Pradesh, India (Vijay et al. 2009) as well as Himachal Pradesh and Tamil Nadu (Ginwal et al. 2009). These studies have clarified that there is a strong need for survey, selection and conservation of genetically divergent genotypes. The present study is an important attempt in this respect and the results show that significant differences exist in all shoot and root-related traits among the seed sources. This genetic variability would be useful for further genetic improvement.

Conclusion

At the age of one and a half years, *A. racemosus* seed sources performed differently at 1% significance level in number of shoots, shoot height, shoot weight, number of roots, root length, root diameter and root weight. Maximum genotypic and pheno-

typic variances were observed in shoot height among the shoot-related traits and root length among the root-related traits. Maximum heritability was observed in root length followed by root weight. The maximum genetic advance and genetic gain were obtained for shoot height among the shoot-related traits and root length among the root-related traits. Index values were developed for all the seed sources based on the four most important traits. Panthnagar (Uttrakhand), followed by Jodhpur (1) (Rajasthan), Dehradun (Uttarakhand), Chandigarh (Punjab), Jammu (Jammu and Kashmir), Jodhpur (2) (Rajasthan) and Solan (Himachal Pradesh), were promising seed sources for root production.

Table 7. Index value for different seed sources

Source No.	Traits				Weightage				Total index value
	No. of shoots	Shoot dry weight (gm)	No. of roots	Root dry weight (gm)	No. of shoots	shoot dry weight	No. of roots	root dry weight	
7	27.00	723.39	129.67	393.81	20	30	20	20	90
1	18.67	635.09	119.33	781.14	5	30	15	30	80
3	21.33	298.18	138.67	1000.81	15	1	20	30	66
6	20.33	568.99	154.00	127.76	10	30	20	1	61
10	29.33	994.41	95.67	251.22	20	30	5	1	56
2	22.33	351.6	116.33	347.22	15	10	15	15	55
13	15.00	310.99	150.67	433.76	1	1	20	30	52
4	15.33	362.2	99.67	591.66	1	10	5	30	46
16	11.00	136.08	110.00	493.07	1	1	10	30	42
8	24.00	359.08	106.00	254.03	20	10	10	1	41
5	17.67	468.81	72.00	156.59	5	30	1	1	37
12	28.33	314.56	112.67	248.64	20	1	15	1	37
19	17.33	483.41	72.67	163.33	5	30	1	1	37
9	17.67	421.88	78.00	286.46	5	20	1	1	27
20	22.00	289.15	101.33	260.79	15	1	10	1	27
11	20.67	145.62	105.67	244.3	10	1	10	1	22
17	13.67	311.69	102.00	271.21	1	1	10	1	13
18	17.33	182.15	70.33	198.75	5	1	1	1	8
14	9.00	20.31	40.50	46.76	1	1	1	1	1
15	13.00	0.77	30.00	16.44	1	1	1	1	1

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